

**Amendments to the Claims**

1. (currently amended) An isolated polynucleotide comprising:
  - (a) a nucleotide sequence encoding a polypeptide having delta-9 fatty acid desaturase activity that has at least 80% identity based on the Clustal method of alignment with default parameters (GAP PENALTY = 10, GAP LENGTH PENALTY = 10) when compared to a polypeptide selected from the group consisting of SEQ ID NO:2; or
  - (b) the complement of (a).
  
2. (currently amended) An isolated polynucleotide comprising:
  - (a) a nucleotide sequence encoding a polypeptide having delta-9 fatty acid desaturase activity that has at least 85% identity based on the Clustal method of alignment with default parameters (GAP PENALTY = 10, GAP LENGTH PENALTY = 10) when compared to a polypeptide selected from the group consisting of SEQ ID NO:2; or
  - (b) the complement of (a).
  
3. (currently amended) An isolated polynucleotide comprising:
  - (a) a nucleotide sequence encoding a polypeptide having delta-9 fatty acid desaturase activity that has at least 90% identity based on the Clustal method of alignment with default parameters (GAP PENALTY = 10, GAP LENGTH PENALTY = 10) when compared to a polypeptide selected from the group consisting of SEQ ID NO:2; or
  - (b) the complement of (a).
  
4. (currently amended) An isolated polynucleotide comprising:
  - (a) a nucleotide sequence encoding a polypeptide having delta-9 fatty acid desaturase activity that has at least 95% identity based on the Clustal method of alignment with default parameters (GAP PENALTY = 10, GAP LENGTH PENALTY = 10) when compared to a polypeptide selected from the group consisting of SEQ ID NO:2; or
  - (b) the complement of (a).
  
5. (currently amended) The isolated polynucleotide of any of Claims 1-4, wherein the nucleotide sequence comprises a nucleic acid sequence selected from the group consisting of SEQ ID NO:1.

6. (original) A chimeric construct comprising the isolated polynucleotide of any of Claims 1-4 operably linked to at least one suitable regulatory sequence.

7. (original) A chimeric construct comprising the isolated polynucleotide of Claim 5 operably linked to at least one suitable regulatory sequence.

8. (original) A host cell comprising the chimeric construct of Claim 6.

9. (original) A host cell comprising the chimeric construct of Claim 7.

10. (withdrawn) A method of obtaining a nucleic acid fragment encoding a delta-9 fatty acid desaturase polypeptide comprising the steps of:

- (a) probing a cDNA or genomic library with an isolated polynucleotide comprising at least one of 30 contiguous nucleotides derived from a nucleotide sequence selected from the group consisting of SEQ ID NO:1, 3, 5, 7, 9, 11, 13, or 15 and/or a complement of the nucleotide sequence;
- (b) identifying a DNA clone that hybridizes with the isolated polynucleotide;
- (c) isolating the identified DNA clone; and
- (d) sequencing a cDNA or genomic fragment that comprises the isolated DNA clone.

11. (withdrawn) A method of obtaining a nucleic acid fragment encoding a delta-9 fatty acid desaturase polypeptide comprising the steps of:

- (a) probing a cDNA or genomic library with an isolated polynucleotide comprising at least one of 30 contiguous nucleotides derived from a nucleotide sequence selected from the group consisting of SEQ ID NO:1, 3, 5, 7, 9, 11, 13, or 15 and/or a complement of such nucleotide sequences;
- (b) identifying a DNA clone that hybridizes with the isolated polynucleotide;
- (c) isolating the identified DNA clone;
- (d) inserting the DNA clone into a plasmid suitable for expression in a bacterial or yeast cell; and
- (e) assaying for delta-9 desaturase activity or alterations in fatty acid composition of the host cell.

12. (withdrawn) A method of identifying an isolated polynucleotide that encodes a delta-9 fatty acid desaturase comprising the steps of:

- (a) determining an amino acid sequence of the polypeptide encoded by the isolated DNA;
- (b) determining if the amino acid sequence comprises at least two amino acid sequences selected from the group consisting of HSMPPPEK corresponding to amino acids 67-73 of SEQ ID NO:2, LPLLKPVE corresponding to amino acids 89-96 of SEQ ID NO:2, EYFVVLVGDM corresponding to amino acids 132-141 of SEQ ID NO:2, EKTU corresponding to amino acids 205-208 of SEQ ID NO:2, GMDPGT corresponding to amino acids 215-220 of SEQ ID NO:2, NNPYLGFVYTSFQERAT corresponding to amino acids 222-238 of SEQ ID NO:2, VLAR corresponding to amino acids 256-259 of SEQ ID NO:2, RIVE corresponding to amino acids 277-280 of SEQ ID NO:2, ITMPAHL corresponding to amino acids 302-308 of SEQ ID NO:2, or DFVCGLA corresponding to amino acids 364-370 of SEQ ID NO:2.

13. (withdrawn) A method of identifying an isolated polynucleotide that encodes a delta-9 fatty acid desaturase comprising the steps of:

- (a) determining the polypeptide sequence of Claim 10, 11, or 12;
- (b) determining that the amino acid sequence of the polypeptide does not contain at least one of the following amino acid sequences KEIPDDYFVVLVGDMITEEALPTYQTMLNT corresponding to positions 116-145 of SEQ ID NO:23; or DYADILEFLVGRWK corresponding to positions 324-337 of SEQ ID NO:23.

14. (original) A method of altering the level of expression of a delta-9 fatty acid desaturase in a host cell comprising:

- (a) transforming a host cell with the chimeric gene of Claim 6; and
- (b) growing the transformed host cell produced in step (a) under conditions that are suitable for expression of the chimeric construct wherein expression of the chimeric construct results in production of altered levels of a delta-9 fatty acid desaturase in the transformed host cell.

15. (original) A method of altering the level of expression of a delta-9 fatty acid desaturase in a host cell comprising:

- (a) transforming a host cell with the chimeric construct of Claim 6 ; and
- (b) growing the transformed host cell produced in step (a) under conditions that are suitable for expression of the chimeric construct wherein expression of the chimeric gene results in production of altered levels of a delta-9 fatty acid desaturase in the transformed host cell.